

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/944,862

DATE: 12/10/2001
TIME: 15:41:35

Input Set : N:\paola\09944862.txt
Output Set: N:\CRF3\12102001\I944862.raw

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1-22-02

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TECH CENTER 1600/2900

ENTERED

3 <110> APPLICANT: Baker, Kevin
4 Botstein, David
5 Eaton, Dan
6 Ferrara, Napoleone
7 Filvaroff, Ellen
8 Gerritsen, Mary
9 Goddard, Audrey
10 Godowski, Paul
11 Grimaldi, Christopher
12 Gurney, Austin
13 Hillan, Kenneth
14 Kljavin, Ivar
15 Napier, Mary
16 Roy, Margaret
17 Tumas, Daniel
18 Wood, William
20 <120> TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
21 ACIDS ENCODING THE SAME
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60 <150> PRIOR APPLICATION NUMBER: 60/070,440
W--> 61 <151> PRIOR FILING DATE: January 5, 1998
63 <150> PRIOR APPLICATION NUMBER: 60/074,086
W--> 64 <151> PRIOR FILING DATE: February 9, 1998

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138 <160> NUMBER OF SEQ ID NOS: 120

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142 <212> TYPE: DNA
143 <213> ORGANISM: Homo Sapien
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150 ctcatctttt cttcttacac agtgtctgag aacatttaca ttatagataa 150
152 gtagtacatg gtggataact tctactttta ggaggactac tctcttctga 200
154 cagtcctaga ctgggtcttct acactaagac accatgaagg agtatgtgct 250
156 cctattattc ctggctttgt gctctgccaa acccttcttt agcccttcac 300
158 acatcgcact gaagaatatg atgctgaagg atatggaaga cacagatgat 350
160 gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
162 tccaacaaga gagccaagaa gccatttttt tccatttgat ctgtttccaa 450
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174 gtcccacaat caactaagtg aaataccact taatcttccc aaatcattag 750
176 cagaactcag aattcatgaa aataaagtta agaaaataca aaaggacaca 800
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230 cgcattttta tgatccgcta ttataagctt ttaatagcat gaaaattggt 2150
232 aggctatata acattgccac ttcaactcta aggaatattt ttgagatata 2200

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236 aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300
238 tagtataact gaataagcag agcatcaaat taaacagaca gaaaccgaaa 2350
240 gctctatata aatgctcaga gttctttatg tattttttat tggcattcaa 2400
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244 aaat 2454
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256                      20                      25                      30
258 Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
259                      35                      40                      45
261 Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
262                      50                      55                      60
264 Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
265                      65                      70                      75
267 Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
268                      80                      85                      90
270 Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
271                      95                      100                     105
273 Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
274                      110                     115                     120
276 Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
277                      125                     130                     135
279 Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
280                      140                     145                     150
282 Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
283                      155                     160                     165
285 Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
286                      170                     175                     180
288 Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
289                      185                     190                     195
291 Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
292                      200                     205                     210
294 Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His Ile Arg
295                      215                     220                     225
297 Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu Pro Pro
298                      230                     235                     240
300 Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser Thr Val
301                      245                     250                     255
303 Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg Leu Gly
304                      260                     265                     270
306 Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser Leu Ala
307                      275                     280                     285

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309 Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn Lys Leu
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312 Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu Gln Ile
313                305                310                315
315 Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val Asn Asp
316                320                325                330
318 Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr Ser Ala
319                335                340                345
321 Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met Gln Pro
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324 Ala Thr Phe Arg Cys Val Leu Ser Arg Met Ser Val Gln Leu Gly
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333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
338 <400> SEQUENCE: 3
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358 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
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365 <212> TYPE: DNA
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373 cctccctccc tctcccccag ctgtcccggt cgcgtcatgc cgagcctccc 150
375 ggccccgcgg gccccgctgc tgcctcctcg gctgctgctg ctcggctccc 200
377 ggccggcccc cggcgccggc ccagagcccc ccgtgctgcc catccgttct 250
379 gagaaggagc cgctgcccgt tcggggagcg gcaggctgca ccttcggcgg 300
381 gaaggtctat gccttggacg agacgtggca cccggaccta gggcagccat 350

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VERIFICATION SUMMARY

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DATE: 12/10/2001

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Output Set: N:\CRF3\12102001\I944862.raw

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